



109700DIVofficeactionSeq.ST25.txt
SEQUENCE LISTING

<110> Asakura, Akira
Hoshino, Tatsuo
Ojima, Setsuko
Shinjo, Masako
Tomiya, Noribumi

<120> Novel Alcohol/Aldehyde Dehydrogenases

<130> C38435/109700CON

<140> 09/470,667

<141> 1999-12-22

<150> US 08/934,506

<151> 1997-09-19

<160> 16

<170> PatentIn version 3.3

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<212> DNA

<213> Gluconobacter oxydans

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Glu Asn Tyr Arg His Ser Pro Leu Thr Gln Ile Thr Thr Glu Asn Val
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Gly Gln Leu Gln Leu Val Trp Ala Arg Gly Met Gln Pro Gly Lys Val
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Gln Val Thr Pro Leu Ile His Asp Gly Val Met Tyr Leu Ala Asn Pro
 Page 5

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 Glu His Arg Arg Gln Leu Pro Asn Ile Ala Thr Leu Asn Ser Phe Gly
 115 120 125
 Glu Pro Thr Arg Gly Met Ala Leu Tyr Gly Thr Asn Val Tyr Phe Val
 130 135 140
 Ser Trp Asp Asn His Leu Val Ala Leu Asp Thr Ala Thr Gly Gln Val
 145 150 155 160
 Thr Phe Asp Val Asp Arg Gly Gln Gly Glu Asp Met Val Ser Asn Ser
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 Gln Tyr Ser Pro Phe Gly Cys Phe Val Ser Gly His Asp Ser Ala Thr
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 Gly Glu Glu Leu Trp Arg Asn Tyr Phe Ile Pro Arg Ala Gly Glu Glu
 210 215 220
 Gly Asp Glu Thr Trp Gly Asn Asp Tyr Glu Ala Arg Trp Met Thr Gly
 225 230 235 240
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 Gly Gly Thr Leu Tyr Gly Thr Asn Thr Arg Phe Ala Val Arg Pro Asp
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 Thr Gly Glu Ile Val Trp Arg His Gln Thr Leu Pro Arg Asp Asn Trp
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 Asp Gln Glu Cys Thr Phe Glu Met Met Val Thr Asn Val Asp Val Gln
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Thr Asn Tyr Gln Asn Met Ile Glu Ser Ile Asp Glu Asn Gly Ile Val
370 375 380

Thr Val Asn Glu Asp Ala Ile Leu Lys Glu Leu Asp Val Glu Tyr Asp
385 390 395 400

Val Cys Pro Thr Phe Leu Gly Gly Arg Asp Trp Pro Ser Ala Ala Leu
405 410 415

Asn Pro Asp Ser Gly Ile Tyr Phe Ile Pro Leu Asn Asn Val Cys Tyr
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Asp Met Met Ala Val Asp Gln Glu Phe Thr Ser Met Asp Val Tyr Asn
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Thr Ser Asn Val Thr Lys Leu Pro Pro Gly Lys Asp Met Ile Gly Arg
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Thr Gly Glu Thr Leu Trp Gln Thr Arg Leu Ala Thr Val Ala Ser Gly
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Gln Ala Ile Ser Tyr Glu Val Asp Gly Met Gln Tyr Val Ala Ile Ala
530 535 540

Gly Gly Gly Val Ser Tyr Gly Ser Gly Leu Asn Ser Ala Leu Ala Gly
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Leu Pro Gln

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 35 40 45

Glu Asn Tyr Arg His Ser Pro Leu Thr Gln Ile Thr Thr Glu Asn Val
 50 55 60

Gly Gln Leu Gln Leu Val Trp Ala Arg Gly Met Gln Pro Gly Lys Val
 65 70 75 80

Gln Val Thr Pro Leu Ile His Asp Gly Val Met Tyr Leu Ala Asn Pro
 85 90 95

Gly Asp Val Ile Gln Ala Ile Asp Ala Lys Thr Gly Asp Leu Ile Trp
 100 105 110

Glu His Arg Arg Gln Leu Pro Asn Ile Ala Thr Leu Asn Ser Phe Gly
 115 120 125

Glu Pro Thr Arg Gly Met Ala Leu Tyr Gly Thr Asn Val Tyr Phe Val
 130 135 140

Ser Trp Asp Asn His Leu Val Ala Leu Asp Thr Ala Thr Gly Gln Val
 145 150 155 160

Thr Phe Asp Val Asp Arg Gly Gln Gly Glu Asp Met Val Ser Asn Ser
 165 170 175

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 180 185 190

Gln Tyr Ser Pro Phe Gly Cys Phe Val Ser Gly His Asp Ser Ala Thr
 195 200 205

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Gly Asp Glu Thr Trp Gly Asn Asp Tyr Glu Ala Arg Trp Met Thr Gly
225 230 235 240

Val Trp Gly Gln Ile Thr Tyr Asp Pro Val Gly Gly Leu Val His Tyr
245 250 255

Gly Ser Ser Ala Val Gly Pro Ala Ser Glu Thr Gln Arg Gly Thr Thr
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Gly Gly Thr Met Tyr Gly Thr Asn Thr Arg Phe Ala Val Arg Pro Glu
275 280 285

Thr Gly Glu Ile Val Trp Arg His Gln Thr Leu Pro Arg Asp Asn Trp
290 295 300

Asp Gln Glu Cys Thr Phe Glu Met Met Val Ala Asn Val Asp Val Gln
305 310 315 320

Pro Ala Ala Asp Met Asp Gly Val Arg Ser Ile Asn Pro Asn Ala Ala
325 330 335

Thr Gly Glu Arg Arg Val Leu Thr Gly Val Pro Cys Lys Thr Gly Thr
340 345 350

Met Trp Gln Phe Asp Ala Glu Thr Gly Glu Phe Leu Trp Ala Arg Asp
355 360 365

Thr Ser Tyr Glu Asn Ile Ile Glu Ser Ile Asp Glu Asn Gly Ile Val
370 375 380

Thr Val Asp Glu Ser Lys Val Leu Thr Glu Leu Asp Thr Pro Tyr Asp
385 390 395 400

Val Cys Pro Leu Leu Leu Gly Gly Arg Asp Trp Pro Ser Ala Ala Leu
405 410 415

Asn Pro Asp Thr Gly Ile Tyr Phe Ile Pro Leu Asn Asn Thr Cys Met
420 425 430

Asp Ile Glu Ala Val Asp Gln Glu Phe Ser Ser Leu Asp Val Tyr Asn
435 440 445

Gln Ser Leu Thr Ala Lys Met Ala Pro Gly Lys Glu Leu Val Gly Arg
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450

Ile Asp Ala Ile Asp Ile Ser Thr Gly Arg Thr Leu Trp Thr Ala Glu
465 470 475 480

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485 490 495

Leu Phe Asn Gly Gly Thr Asp Arg Tyr Phe Arg Ala Leu Ser Gln Glu
500 505 510

Thr Gly Glu Thr Leu Trp Gln Thr Arg Leu Ala Thr Val Ala Ser Gly
515 520 525

Gln Ala Val Ser Tyr Glu Ile Asp Gly Val Gln Tyr Ile Ala Ile Gly
530 535 540

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Pro Gln Gln

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35 40 45

Asn Tyr Arg His Ser Pro Leu Thr Gln Ile Thr Ala Asp Asn Val Gly
50 55 60

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100 105 110

His Arg Arg Gln Leu Pro Asn Ile Ala Thr Leu Asn Ser Phe Gly Glu
115 120 125

Pro Thr Arg Gly Met Ala Leu Tyr Gly Thr Asn Val Tyr Phe Val Ser
130 135 140

Trp Asp Asn His Leu Val Ala Leu Asp Thr Ser Thr Gly Gln Val Val
145 150 155 160

Phe Asp Val Asp Arg Gly Gln Gly Thr Asp Met Val Ser Asn Ser Ser
165 170 175

Gly Pro Ile Val Ala Asn Gly Val Ile Val Ala Gly Ser Thr Cys Gln
180 185 190

Tyr Ser Pro Phe Gly Cys Phe Val Ser Gly His Asp Ser Ala Thr Gly
195 200 205

Glu Glu Leu Trp Arg Asn Thr Phe Ile Pro Arg Ala Gly Glu Glu Gly
210 215 220

Asp Glu Thr Trp Gly Asn Asp Tyr Glu Ala Arg Trp Met Thr Gly Val
225 230 235 240

Trp Gly Gln Ile Thr Tyr Asp Pro Val Gly Gly Leu Val His Tyr Gly
245 250 255

Thr Ser Ala Val Gly Pro Ala Ala Glu Ile Gln Arg Gly Thr Val Gly
260 265 270

Gly Ser Met Tyr Gly Thr Asn Thr Arg Phe Ala Val Arg Pro Glu Thr
275 280 285

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290 295 300

Gln Glu Cys Thr Phe Glu Met Met Val Val Asn Val Asp Val Gln Pro
305 310 315 320

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325 330 335

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340 345 350

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355 360 365

Ser Tyr Gln Asn Leu Ile Glu Ser Val Asp Pro Asp Gly Leu Val His
370 375 380

Val Asn Glu Asp Leu Val Val Thr Glu Leu Glu Val Ala Tyr Glu Ile
385 390 395 400

Cys Pro Thr Phe Leu Gly Gly Arg Asp Trp Pro Ser Ala Ala Leu Asn
405 410 415

Pro Asp Thr Gly Ile Tyr Phe Ile Pro Leu Asn Asn Ala Cys Ser Gly
420 425 430

Met Thr Ala Val Asp Gln Glu Phe Ser Ser Leu Asp Val Tyr Asn Val
435 440 445

Ser Leu Asp Tyr Lys Leu Ser Pro Gly Ser Glu Asn Met Gly Arg Ile
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Asp Ala Ile Asp Ile Ser Thr Gly Arg Thr Leu Trp Ser Ala Glu Arg
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Tyr Ala Ser Asn Tyr Ala Pro Val Leu Ser Thr Gly Gly Gly Val Leu
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Gly Glu Thr Leu Trp Gln Thr Arg Leu Ala Thr Val Ala Ser Gly Gln
515 520 525

Ala Ile Ser Tyr Glu Ile Asp Gly Val Gln Tyr Val Ala Ile Gly Arg
530 535 540

Gly Gly Thr Ser Tyr Gly Ser Asn His Asn Arg Ala Leu Thr Glu Arg
545 550 555 560

Ile Asp Ser Thr Ala Ile Gly Ser Ala Ile Tyr Val Phe Ala Leu Pro
565 570 575

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Gln Gln

<210> 8
 <211> 579
 <212> PRT
 <213> Gluconobacter oxydans

<220>
 <221> SIGNAL
 <222> (1)..(23)

<400> 8

Met Asn Pro Thr Thr Leu Leu Arg Thr Ser Ala Ala Val Leu Leu Leu
 1 5 10 15

Thr Ala Pro Ala Ala Phe Ala Gln Val Thr Pro Ile Thr Asp Glu Leu
 20 25 30

Leu Ala Asn Pro Pro Ala Gly Glu Trp Ile Asn Tyr Gly Arg Asn Gln
 35 40 45

Glu Asn Tyr Arg His Ser Pro Leu Thr Gln Ile Thr Ala Asp Asn Val
 50 55 60

Gly Gln Leu Gln Leu Val Trp Ala Arg Gly Met Glu Ala Gly Ala Val
 65 70 75 80

Gln Val Thr Pro Met Ile His Asp Gly Val Met Tyr Leu Ala Asn Pro
 85 90 95

Gly Asp Val Ile Gln Ala Leu Asp Ala Gln Thr Gly Asp Leu Ile Trp
 100 105 110

Glu His Arg Arg Gln Leu Pro Ala Val Ala Thr Leu Asn Ala Gln Gly
 115 120 125

Asp Arg Lys Arg Gly Val Ala Leu Tyr Gly Thr Ser Leu Tyr Phe Ser
 130 135 140

Ser Trp Asp Asn His Leu Ile Ala Leu Asp Met Glu Thr Gly Gln Val
 145 150 155 160

Val Phe Asp Val Glu Arg Gly Ser Gly Glu Asp Gly Leu Thr Ser Asn
 165 170 175

Thr Thr Gly Pro Ile Val Ala Asn Gly Val Ile Val Ala Gly Ser Thr

180 Cys Gln Tyr Ser Pro Tyr Gly Cys Phe Ile Ser Gly His Asp Ser Ala
 195 200 205
 Thr Gly Glu Glu Leu Trp Arg Asn His Phe Ile Pro Gln Pro Gly Glu
 210 215 220
 Glu Gly Asp Glu Thr Trp Gly Asn Asp Phe Glu Ala Arg Trp Met Thr
 225 230 235 240
 Gly Val Trp Gly Gln Ile Thr Tyr Asp Pro Val Thr Asn Leu Val Phe
 245 250 255
 Tyr Gly Ser Thr Gly Val Gly Pro Ala Ser Glu Thr Gln Arg Gly Thr
 260 265 270
 Pro Gly Gly Thr Leu Tyr Gly Thr Asn Thr Arg Phe Ala Val Arg Pro
 275 280 285
 Asp Thr Gly Glu Ile Val Trp Arg His Gln Thr Leu Pro Arg Asp Asn
 290 295 300
 Trp Asp Gln Glu Cys Thr Phe Glu Met Met Val Ala Asn Val Asp Val
 305 310 315 320
 Gln Pro Ser Ala Glu Met Glu Gly Leu Arg Ala Ile Asn Pro Asn Ala
 325 330 335
 Ala Thr Gly Glu Arg Arg Val Leu Thr Gly Ala Pro Cys Lys Thr Gly
 340 345 350
 Thr Met Trp Ser Phe Asp Ala Ala Ser Gly Glu Phe Leu Trp Ala Arg
 355 360 365
 Asp Thr Asn Tyr Thr Asn Met Ile Ala Ser Ile Asp Glu Thr Gly Leu
 370 375 380
 Val Thr Val Asn Glu Asp Ala Val Leu Lys Glu Leu Asp Val Glu Tyr
 385 390 395 400
 Asp Val Cys Pro Thr Phe Leu Gly Gly Arg Asp Trp Ser Ser Ala Ala
 405 410 415
 Leu Asn Pro Asp Thr Gly Ile Tyr Phe Leu Pro Leu Asn Asn Ala Cys
 420 425 430

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Tyr Asp Ile Met Ala Val Asp Gln Glu Phe Ser Ala Leu Asp Val Tyr
435 440 445

Asn Thr Ser Ala Thr Ala Lys Leu Ala Pro Gly Phe Glu Asn Met Gly
450 455 460

Arg Ile Asp Ala Ile Asp Ile Ser Thr Gly Arg Thr Leu Trp Ser Ala
465 470 475 480

Glu Arg Pro Ala Ala Asn Tyr Ser Pro Val Leu Ser Thr Ala Gly Gly
485 490 495

Val Val Phe Asn Gly Gly Thr Asp Arg Tyr Phe Arg Ala Leu Ser Gln
500 505 510

Glu Thr Gly Glu Thr Leu Trp Gln Ala Arg Leu Ala Thr Val Ala Thr
515 520 525

Gly Gln Ala Ile Ser Tyr Glu Leu Asp Gly Val Gln Tyr Ile Ala Ile
530 535 540

Gly Ala Gly Gly Leu Thr Tyr Gly Thr Gln Leu Asn Ala Pro Leu Ala
545 550 555 560

Glu Ala Ile Asp Ser Thr Ser Val Gly Asn Ala Ile Tyr Val Phe Ala
565 570 575

Leu Pro Gln

<210> 9
<211> 82
<212> DNA
<213> synthetic oligonucleotide

<400> 9
catgaaaata aaaacaggtg cacgcatcct cgcattatcc gcattaacga cgatgatgtt 60
ttccgcctcg gctctcgccc ag 82

<210> 10
<211> 83
<212> DNA
<213> synthetic oligonucleotide

<400> 10
gttacctggg cgagagccga ggcggaaaac atcatcgtcg ttaatgcgga taatgcgagg 60
atgcgtgcac ctgtttttat ttt 83

<210> 11

109700DIVofficeactionSeq.ST25.txt

<211> 27
<212> PRT
<213> Escherichia coli

<220>
<221> SIGNAL
<222> (1)..(26)

<400> 11

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
1 5 10 15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Gln
20 25

<210> 12
<211> 27
<212> DNA
<213> synthetic oligonucleotide

<400> 12
gttagcgcgg tggatcccca ttggagg

27

<210> 13
<211> 24
<212> DNA
<213> oligonucleotide probe

<400> 13
atgatggtga tcacgatcaa tcgt

24

<210> 14
<211> 13
<212> PRT
<213> Gluconobacter oxydans

<400> 14

Met Met Val Thr Asn Val Asp Val Gln Met Ser Thr Glu
1 5 10

<210> 15
<211> 6
<212> PRT
<213> Pseudomonas putida

<400> 15

Gln Val Thr Pro Val Thr
1 5

<210> 16
<211> 11
<212> PRT
<213> Pseudomonas putida

109700DIVofficeactionSeq.ST25.txt

<400> 16

Gln Val Thr Pro Ile Thr Asp Glu Leu Leu Ala
1 5 10